

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: April 26, 2005, 11:09:29 ; Search time 13.2396 Seconds  
(without alignments)  
6706.854 Million cell updates/sec

Title: US-10-750-965-40

Perfect score: 15

Sequence: 1 gaacagatcttga 15

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : N\_Geneseq\_16Dec04:\*

- 1: Geneseq1980s:\*
- 2: Geneseq1990s:\*
- 3: Geneseq2000s:\*
- 4: Geneseq2001as:\*
- 5: Geneseq2001bs:\*
- 6: Geneseq2002as:\*
- 7: Geneseq2002bs:\*
- 8: Geneseq2003as:\*
- 9: Geneseq2003bs:\*
- 10: Geneseq2003cs:\*
- 11: Geneseq2003ds:\*
- 12: Geneseq2004as:\*
- 13: Geneseq2004bs:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	15	100.0	15	AAA07571	AAa07571 Detoxifile
2	15	100.0	322	AD171247	AD171247 Human ova
3	15	100.0	322	AD136407	AD136407 Human ova
4	15	100.0	385	AD142791	AD142791 Human ova
5	15	100.0	556	AD142842	AD142842 Human ova
6	15	100.0	672	AAK84821	AAK84821 Human imm
7	15	100.0	672	AAK63395	AAK63395 Human imm
8	15	100.0	877	AD162798	AD162798 Human ova
9	15	100.0	1845	AAAC45833	AAAC45833 Arabidops
10	15	100.0	1939	ABX70923	ABX70923 Arabidops
11	15	100.0	1945	AAAC44652	AAAC44652 Arabidops
12	15	100.0	3972	ABZ14299	ABZ14299 Arabidops
13	15	100.0	11	ACN44506	ACn44506 Human, gen
14	15	93.3	181	AAZ122830	AAZ122830 Human sec
15	15	93.3	300	AAZ14242	AAZ14242 Human gen
16	15	93.3	300	AAZ98669	AAZ98669 Human can
17	15	93.3	314	AAZ75535	AAZ75535 DNA encod
18	15	93.3	341	AAZ67219	AAZ67219 Novel hum
19	15	93.3	372	ACD95670	ACD95670 Human col
20	15	93.3	381	AAZ67260	AAZ67260 Novel hum

# ALIGNMENTS

21	14	93.3	384	6	ABN76896	ABn76896 Human ORF
22	14	93.3	431	8	ABX62031	ABx62031 Arabidops
23	14	93.3	466	6	AB193530	AB193530 Arabidops
24	14	93.3	483	9	ACH18421	ACH18421 Human adu
25	14	93.3	610	5	ADL36458	ADl36458 Human ova
26	14	93.3	610	5	AD171298	ADl71298 Human ova
27	14	93.3	612	8	ACA39967	ACA39967 Prokaryot
28	14	93.3	618	3	AAAC10902	AAAC10902 Human sec
29	14	93.3	623	5	AAH58846	AAH58846 Human SCN
30	14	93.3	737	2	AAZ98728	AAZ98728 Human val
31	14	93.3	744	8	ACA53032	ACA53032 Prokaryot
32	14	93.3	745	3	AAAC10881	AAAC10881 Human sec
33	14	93.3	777	5	AAZ75537	AAZ75537 DNA encod
34	14	93.3	834	4	ABA89060	ABA89060 Escherich
35	14	93.3	960	10	ADH85067	ADH85067 Enterococ
36	14	93.3	1225	6	ABK35807	ABK35807 cDNA sequ
37	14	93.3	1336	6	ABQ54665	ABQ54665 Human ova
38	14	93.3	1357	10	ADC64340	ADC64340 HYP4 codi
39	14	93.3	1421	4	AAZ02046	AAZ02046 DNA encod
40	14	93.3	1448	2	AAO40202	AAO40202 Sequence
41	14	93.3	1457	13	ADS50509	ADS50509 Bacterial
42	14	93.3	1465	4	AA160558	AA160558 Human pol
43	14	93.3	1467	4	AA158772	AA158772 Human pol
44	14	93.3	1467	5	ADQ98992	ADQ98992 DNA encod
45	14	93.3	1467	9	ADB48752	ADB48752 Novel hum

# RESULT 1

AA07571 standard; DNA, 15 BP.

AA07571;

29-AUG-2000 (first entry)

Detoxified Shiga toxin 2 modified segment #4.

Expression cassette; plasmid maintenance system; Neisseria meningitidis; post-segregational killing function; ompC promoter; immune response; vaccine; Salmonella typhi; hepatitis; Haemophilus influenzae type b; acellular pertussis; varicella; rotavirus; Streptococcus pneumoniae; cancer vaccine; autoimmune disorder; immunological disease; allergy; myasthenia gravis; lupus erythematosus; rheumatoid arthritis; therapy; multiple sclerosis; asthma; ss.

Salmonella typhi.

WO200032047-A1.

08-JUN-2000.

02-DEC-1999; 99WC-US028499.

02-DEC-1998; 98US-00204117.

12-OCT-1999; 99US-0158738P.

(UYMA-) UNIV MARYLAND BALTIMORE.

Galen JE;

WPI; 2000-412091/35.

Expression cassette used as live vector vaccine comprises nucleotide sequence encoding origin of replication and plasmid maintenance system which includes a post-segregational killing and a partitioning function.

Claim 32; Page 92; 127pp; English.

This sequence is a modified Shiga 2 toxin fragment and can be used in the expression cassette of the invention. The cassette is an independently

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Run on: April 26, 2005, 11:14:05 / Search time 83.643 Seconds  
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8689.645 Million cell updates/sec

Title: US-10-750-965-39

Perfect score: 15

Sequence: 1 gaattcgaccact 15

Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: GenEmbl.\*  
1: gb Da.\*  
2: gb Htg.\*  
3: gb In.\*  
4: gb Om.\*  
5: gb Ov.\*  
6: gb Pac.\*  
7: gb Ph.\*  
8: gb Pl.\*  
9: gb Pr.\*  
10: gb Ro.\*  
11: gb Str.\*  
12: gb Sy.\*  
13: gb Un.\*  
14: gb Vi.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	15	100.0	1924	9 AK129669	AK129669 Homo sapi
2	15	100.0	3137	8 NC0243517	AJ243517 Neurospor
3	15	100.0	3566	9 EX119906	EX119906 Human DNA
4	15	100.0	17966	2 AC138145	AC138145 Homo sapi
5	15	100.0	190107	9 AC100832	AC100832 Homo sapi
6	15	100.0	349841	1 BX572606	BX572606 Rhodosphe
7	15	93.3	385	6 CO472848	CO472848 Sequence
8	14	93.3	396	6 CO478754	CO478754 Sequence
9	14	93.3	417	6 CO465586	CO465586 Sequence
10	14	93.3	428	6 CO482017	CO482017 Sequence
11	14	93.3	430	6 CO503156	CO503156 Sequence
12	14	93.3	438	6 CO499951	CO499951 Sequence
13	14	93.3	438	6 CO508919	CO508919 Sequence
14	14	93.3	438	6 CO512005	CO512005 Sequence
15	14	93.3	459	6 CO692166	CO692166 Sequence
16	14	93.3	559	6 BD152296	BD152296 Primer fo
17	14	93.3	559	6 AX872234	AX872234 Sequence
18	14	93.3	594	6 CO489052	CO489052 Sequence
19	14	93.3	594	6 CO491123	CO491123 Sequence

c 20	14	93.3	594	6	CO494900	CO494900 Sequence
c 21	14	93.3	594	6	CO496987	CO496987 Sequence
c 22	14	93.3	966	13	AY487538	AY487538 Unculture
c 23	14	93.3	1200	6	AR376947	AR376947 Sequence
c 24	14	93.3	1521	1	AF411070	AF411070 Sphingomo
c 25	14	93.3	1681	9	AK000455	AK000455 Homo sapi
c 26	14	93.3	2133	6	BD159467	BD159467 Primer fo
c 27	14	93.3	2133	6	AX882028	AX882028 Sequence
c 28	14	93.3	2133	6	AK027380	AK027380 Homo sapi
c 29	14	93.3	3075	1	AF127079	AF127079 Salimone11
c 30	14	93.3	7119	3	AF329639	AF329639 Drosophill
c 31	14	93.3	21470	1	AB008733	AB008733 Salimone11
c 32	14	93.3	43596	9	AC091886	AC091886 Homo sapi
c 33	14	93.3	56883	2	AL365182	AL365182 Homo sapi
c 34	14	93.3	60752	2	AC105060	AC105060 Mus muscu
c 35	14	93.3	119184	1	D90909	D90909 Synchocyst
c 36	14	93.3	119638	9	AC024575	AC024575 Homo sapi
c 37	14	93.3	132492	9	AC007616	AC007616 Homo sapi
c 38	14	93.3	142645	9	AC008481	AC008481 Homo sapi
c 39	14	93.3	144000	9	AC007621	AC007621 Homo sapi
c 40	14	93.3	144771	2	AC018610	AC018610 Homo sapi
c 41	14	93.3	152081	9	AC007381	AC007381 Homo sapi
c 42	14	93.3	163049	9	BS000182	BS000182 Pan trogl
c 43	14	93.3	163384	9	AC009180	AC009180 Homo sapi
c 44	14	93.3	164008	2	AC024064	AC024064 Homo sapi
c 45	14	93.3	169250	9	AP002812	AP002812 Homo sapi

## ALIGNMENTS

RESULT 1  
LOCUS AK129669  
DEFINITION Homo sapiens cDNA FLJ26158 fis, clone ADG01579.  
ACCESSION AK129669  
VERSION AK129669.1 GI:34526262  
KEYWORDS cDNA  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

REFERENCE  
AUTHORS Teshiro, H., Yamazaki, M., Watanabe, K., Kumagai, A., Itakura, S.,  
Fukuzumi, Y., Fujimori, Y., Komiyama, M., Suzuki, Y., Hata, H.,  
Nakagawa, K., Mizuno, S., Morinaga, M., Kawamura, M., Sugiyama, T.,  
Irie, R., Otsuki, T., Sato, H., Nishikawa, T., Sugiyama, A.,  
Kawakami, B., Nagai, K., Isogai, T. and Sugano, S.

COMMENT  
TITLE NEDO human cDNA sequencing project  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 1924)  
AUTHORS Sugano, S., and Suzuki, Y.  
JOURNAL Direct Submission

COMMENT  
TITLE Submitted (31-JUL-2003) Sumio Sugano, Institute of Medical Science,  
University of Tokyo, Laboratory of Genome Structure, Human Genome  
Center, Shitokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639, Japan  
(E-mail: flicdn@ims.u-tokyo.ac.jp, Tel:81-3-5449-5286,  
Fax:81-3-5449-5416)  
NEDO human cDNA sequencing project supported by Ministry of  
Economy, Trade and Industry of Japan; cDNA full insert sequencing:  
Research Association for Biotechnology (RAB); cDNA library  
construction and 5'-end one pass sequencing: Institute of Medical  
Science, University of Tokyo; Laboratory of Genome Structure, Human  
Genome Center; 3'-end one pass sequencing: RAB; clone selection for  
full insert sequencing: RAB and Helix Research Institute.

## FEATURES

source  
1. 1924  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="ADG01579"  
/issue\_type="adrenal gland"  
/clone\_lib="ADG"

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OM nucleic - nucleic search, using sw model

Run on: April 26, 2005, 11:14:05 / Search time 6674.71 Seconds  
(without alignments)  
8689.645 Million cell updates/sec

Title: US-10-750-965-2

Perfect score: 1197

Sequence: 1 ctcaacaatgagctagcc.....gacgcagcgcggaagcag 1197

Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: GenBank:  
1: gb\_ha:\*  
2: gb\_hlg:\*  
3: gb\_in:\*  
4: gb\_om:\*  
5: gb\_ov:\*  
6: gb\_pac:\*  
7: gb\_ph:\*  
8: gb\_pl:\*  
9: gb\_pr:\*  
10: gb\_ro:\*  
11: gb\_scs:\*  
12: gb\_sy:\*  
13: gb\_un:\*  
14: gb\_vl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1197	100.0	1197	6	AR483258 Sequence
2	817.4	68.3	1197	6	AR483257 Sequence
3	718.2	60.0	6271	6	AX18406 Sequence
4	718.2	60.0	8908	6	AX18423 Sequence
5	627.4	52.4	1026	1	ECPI5A
6	627.4	52.4	2314	1	AF432497
7	627.4	52.4	2553	12	CVE289102
8	627.4	52.4	2568	12	CVE277764
9	627.4	52.4	3210	12	AF361440
10	627.4	52.4	3465	6	AX000478 Sequence
11	627.4	52.4	3465	6	BD073379 Sequence
12	627.4	52.4	3481	6	AX000480 Sequence
13	627.4	52.4	3481	6	BD073380 Sequence
14	627.4	52.4	3666	12	U66309
15	627.4	52.4	3720	6	BD136661
16	627.4	52.4	3720	6	AX018968 Sequence
17	627.4	52.4	3794	6	BD136662 Sequence
18	627.4	52.4	3794	6	AX000474 Sequence
19	627.4	52.4	3794	6	AX018970 Sequence

c	20	627.4	52.4	3794	6	BD073377	BD073377 Process f
c	21	627.4	52.4	3801	6	AR493833	AR493833 Sequence
c	22	627.4	52.4	3810	6	AX000476	AX000476 Sequence
c	23	627.4	52.4	3810	6	BD073378	BD073378 Process f
c	24	627.4	52.4	4245	6	AR069365	AR069365 Sequence
c	25	627.4	52.4	4245	12	PACYC184	X06403 Cloning vec
c	26	627.4	52.4	4411	6	AR069366	AR069366 Sequence
c	27	627.4	52.4	4753	12	AF129432	AF129432 Cloning v
c	28	627.4	52.4	4975	6	BD136663	BD136663 Process f
c	29	627.4	52.4	4975	6	AX189972	AX189972 Sequence
c	30	627.4	52.4	5077	6	AX799953	AX799953 Sequence
c	31	627.4	52.4	5201	6	AR493834	AR493834 Sequence
c	32	627.4	52.4	5201	6	AR493835	AR493835 Sequence
c	33	627.4	52.4	5635	12	CV047103	U47103 Cloning vec
c	34	627.4	52.4	6101	12	SIN417448	AJ17448 Shuttle 1
c	35	627.4	52.4	6123	12	SIN417449	AJ17449 Shuttle 1
c	36	627.4	52.4	6363	6	AR069367	AR069367 Sequence
c	37	627.4	52.4	6758	12	AF121784	AF121784 Expression
c	38	627.4	52.4	7151	12	AY042185	AY042185 Cloning v
c	39	627.4	52.4	8774	12	IVU69267	IVU69267 Integration
c	40	627.4	52.4	9065	12	AF405698	AF405698 Reporter
c	41	627.4	52.4	12168	12	AF405696	AF405696 Reporter
c	42	627.4	52.4	12248	12	AF405697	AF405697 Reporter
c	43	627.4	52.4	14928	12	AY230218	AY230218 Expression
c	44	627.4	52.4	18658	12	XU073849	U73849 Synthetic t
c	45	626.2	52.3	4523	12	EVE243540	AJ243540 Expression

## ALIGNMENTS

RESULT 1  
AR483258  
LOCUS AR483258 1197 bp DNA linear PAT 14-MAY-2004  
DEFINITION Sequence 2 from patent US 6703233.  
ACCESSION AR483258  
VERSION AR483258.1 GI:47245789  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 1197)  
AUTHORS Galen J.E.  
TITLE Plasmid maintenance system for antigen delivery  
JOURNAL Patent: US 6703233-A 2 09-MAR-2004;  
FEATURES  
source 1. 1197  
/organism="unknown"  
/mol\_type="genomic DNA"

ORIGIN	Query Match	Best Local Similarity	100.0%	Score 1197	DB 6	Length 1197
Matches 1197	Conservative 0	Mismatches 0	Indels 0	Gaps 0		
QY	1	CTACAAATATATAGACTAGCCCGCTTAATGAGCGGCTTTTCTCGGCTTAGAGATA	60			
DB	1	CTACAAATATATAGACTAGCCCGCTTAATGAGCGGCTTTTCTCGGCTTAGAGATA	60			
QY	61	CTTAAACGAGGAGATGAGAGCGCGCGGAAACCGCTTTTCTCATAGCGTCCGCCCTG	120			
DB	61	CTTAAACGAGGAGATGAGAGCGCGCGGAAACCGCTTTTCTCATAGCGTCCGCCCTG	120			
QY	121	ACAAGCATCAGGAATCGAGCGCTCAATCATGCTGCGGCGAAACCCAGACCTATATA	180			
DB	121	ACAAGCATCAGGAATCGAGCGCTCAATCATGCTGCGGCGAAACCCAGACCTATATA	180			
QY	181	GATACACGAGGCTTCCCGCTGCGGCTCCCTCGGCGGCTCCCTGCTTCCCTTCCGT	240			
DB	181	GATACACGAGGCTTCCCGCTGCGGCTCCCTCGGCGGCTCCCTGCTTCCCTTCCGT	240			
QY	241	TTACCGGTGATCTCCGCTGATATAGCGCGGCTTGTCTCATTCAGCCCTGACCTAGT	300			
DB	241	TTACCGGTGATCTCCGCTGATATAGCGCGGCTTGTCTCATTCAGCCCTGACCTAGT	300			

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OM nucleic - nucleic search, using sw model

Run on: April 26, 2005, 16:32:44 ; Search time 9.14085 Seconds  
(without alignments)  
9714.213 Million cell updates/sec

Title: US-10-750-976-38

Perfect score: 15

Sequence: 1 ctgaacctaggcgca 15

Scoring table: IDENTITY NUC  
Gapop 10.0, Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database : N\_Geneseq\_16Dec04:\*

1: geneseqn1980s:\*\n2: geneseqn1908s:\*\n3: geneseqn2000s:\*\n4: geneseqn2001as:\*\n5: geneseqn2001bs:\*\n6: geneseqn2002as:\*\n7: geneseqn2002bs:\*\n8: geneseqn2003as:\*\n9: geneseqn2003bs:\*\n10: geneseqn2003cs:\*\n11: geneseqn2003ds:\*\n12: geneseqn2004as:\*\n13: geneseqn2004bs:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	15	100.0	15	AAA07569	Aaa07569 Detoxifile
2	14	93.3	1296	AAH53040	Aah53040 S. epider
3	14	93.3	1353	ABN92511	Abn92511 Staphyloc
4	14	93.3	1353	ADSO2545	Adso2545 Staphyloc
5	14	93.3	2168	AAO73674	Aao73674 Myctemic
6	14	93.3	3017	AAH55058	Aah55058 S. epider
7	14	93.3	3233	AAH54222	Aah54222 S. epider
8	14	93.3	4185	AAH54282	Aah54282 S. epider
9	13.4	89.3	21	ABZ81298	Abz81298 Human fer
10	13.4	89.3	21	ABZ81297	Abz81297 Human fer
11	13.4	89.3	507	ABO67565	Abg67565 Listeria
12	13.4	89.3	545	ACH38779	Ach38779 Human foe
13	13.4	89.3	546	ABL87574	AbL87574 Human ova
14	13.4	89.3	570	ABN65688	Abn65688 Human can
15	13.4	89.3	1115	ADBE83428	Adbe83428 Human gen
16	13.4	89.3	1115	ADBE8124	Adbe8124 Human gen
17	13.4	89.3	2121	ACA40982	Aca40982 Prokaryot
18	13.4	89.3	2130	ACA41919	Aca41919 Prokaryot
19	13.4	89.3	2208	ABZ40095	Abz40095 N. gonorr
20	13.4	89.3	2584	ADL71054	Adl71054 Gene. enco

21	13.4	89.3	2712	8	ACC77004	Acc77004 Bacillus
22	13.4	89.3	2937	10	ADB61886	Adb61886 Human CDN
23	13.4	89.3	3488	10	ADC30742	Adc30742 Human nov
24	13.4	89.3	3686	12	ADOC3553	Adoc3553 Novel hum
25	13.4	89.3	5650	4	AAH98514	Aah98514 Human EST
26	13.4	89.3	5650	10	ADC32512	Adc32512 Human nov
27	13.4	89.3	7080	12	ADL6747	Adl6747 Human nov
28	13.4	89.3	7404	13	ADRE4264	Adre4264 Aspergill
29	13.4	89.3	10596	10	ACF72013	Acf72013 Phototrab
30	13.4	89.3	14403	4	AAI07146	Aai07146 Human rep
31	13.4	89.3	19183	4	AAK64938	Aak64938 Human imm
32	13.4	89.3	19183	4	AAI36434	Aai36434 Human mus
33	13.4	89.3	19183	8	ABX59422	Abx59422 CDNA enco
34	13.4	89.3	19183	12	ADJ30172	Adj30172 CDNA mus
35	13.4	89.3	32607	11	ACNA43918	Acna43918 Human gen
36	13.4	89.3	32675	11	ACNA4480	Acna4480 Mouse gen
37	13.4	89.3	48275	3	AAAB1501	Aaab1501 N. mening
38	13.4	89.3	110000	3	AAAB1489_0	Aaab1489 N. mening
39	13.4	89.3	110000	6	ABO69245_00	Abg69245 Listeria
40	13.4	89.3	110000	6	ABO69245_01	Abg69245 Listeria
41	13.4	89.3	110000	6	ABO67197_00	Abg67197 Listeria
42	13.4	89.3	110000	10	ACF67367_52	Acf67367 Listeria
43	13.4	89.3	110000	10	ACF65387_3	Acf65387 Listeria
44	13.4	89.3	117574	6	AAI45288	Aai45288 Human KCN
45	13.4	89.3	127767	13	ABD32657	Abd32657 Mouse can

## ALIGNMENTS

RESULT 1	AAA07569	standard; DNA; 15 BP.
ID	AAA07569	
XX	AAA07569;	
XX	29-AUG-2000	(first entry)
DE	Detoxified Shiga toxin 2 modified segment #2.	
XX	Expression cassette; plasmid maintenance system; Neisseria meningitidis;	
KW	post-segregational killing function; ompC promoter; immune response;	
KW	vaccine; Salmonella typhi; hepatitis; Haemophilus influenzae type b;	
KW	cellular pertussis; varicella; rotavirus; Streptococcus pneumoniae;	
KW	cancer vaccine; autoimmune disorder; immunological disease; allergy;	
KW	myasthenia gravis; lupus erythematosus; rheumatoid arthritis; therapy;	
KW	multiple sclerosis; asthma; ss.	
XX	Salmonella typhi.	
XX	OS	
XX	PN	WG0200032047-A1.
XX	PD	08-JUN-2000.
XX	PF	02-DEC-1999; 99MO-US028499.
XX	PR	02-DEC-1998; 98US-00204117.
XX	PR	12-OCT-1999; 99US-0158738P.
XX	PA	(UYMA-) UNIV MARYLAND BALTIMORE.
XX	PI	Galen JB;
XX	DR	WPI; 2000-412091/35.
XX	PT	Expression cassette used as live vector vaccine comprises nucleotide
XX	PT	sequence encoding origin of replication and plasmid maintenance system
XX	XX	which includes a post-segregational killing and a partitioning function.
PS	Claim 32, Page 92, 127pp, English.	
CC	This sequence is a modified Shiga 2 toxin fragment and can be used in the	
CC	expression cassette of the invention. The cassette is an independently	

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Run on: April 26, 2005, 18:04:09 ; Search time 69.3063 Seconds  
(without alignments)  
10487.183 Million cell updates/sec

Title: US-10-750-976-37

Perfect score: 15

Sequence: 1 acagcagacgcgtta 15

Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : GenEmbl.\*  
1: gb\_da.\*  
2: gb\_hcg.\*  
3: gb\_in.\*  
4: gb\_om.\*  
5: gb\_ov.\*  
6: gb\_pac.\*  
7: gb\_ph.\*  
8: gb\_pl.\*  
9: gb\_pr.\*  
10: gb\_ro.\*  
11: gb\_rtg.\*  
12: gb\_sy.\*  
13: gb\_un.\*  
14: gb\_vl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	15	100.0	3959	14	AY547458 Avian ort
2	15	100.0	211113	2	CR391962 Dario rer
3	14	93.3	714	9	HS437219
4	14	93.3	3312	3	AY433803 Trypanoso
5	14	93.3	5069	5	AF038560 Gallus ga
6	14	93.3	10221	1	AE014558 Brucella
7	14	93.3	10495	1	AE009700 Brucella
8	14	93.3	24523	1	AE008756 Brucella
9	14	93.3	36748	7	AY539836 Burkholde
10	14	93.3	39949	3	AC008782 Burkholde
11	14	93.3	106256	3	AC108135 Leishmani
12	14	93.3	110000	2	AP006498 7
13	14	93.3	133713	3	AC087838 Leishmani
14	14	93.3	147226	9	AC103736 Homo sapi
15	14	93.3	152770	9	AC013602 Homo sapi
16	14	93.3	173839	9	AC026005 Homo sapi
17	14	93.3	181097	2	AC118205 Mus muscu
18	14	93.3	217285	2	AC126317 Rattus no
19	14	93.3	233050	1	AL627271 Saimonelli

C 20	14	93.3	260760	2	AC127861 Rattus no
C 21	14	93.3	295050	1	AL591982 Listeria
C 22	14	93.3	300523	1	AE016838 Saimonelli
C 23	14	93.3	305325	1	AE016765 Escherich
C 24	14	93.3	311600	1	AE016871 Pseudomon
C 25	14	93.3	340750	1	BX294135 Pirellula
C 26	14	93.3	349980	6	AX641671 Sequence
C 27	13.4	89.3	155	8	HV19R
C 28	13.4	89.3	227	8	HVE13231R
C 29	13.4	89.3	231	8	HVE13231R
C 30	13.4	89.3	232	8	HVE1324NR
C 31	13.4	89.3	243	6	AR321328
C 32	13.4	89.3	318	6	AX048488
C 33	13.4	89.3	318	6	AX048488
C 34	13.4	89.3	356	8	HVE08492R
C 35	13.4	89.3	413	6	CO481384
C 36	13.4	89.3	640	14	AF322856
C 37	13.4	89.3	798	6	AR388811
C 38	13.4	89.3	817	8	PSU58023
C 39	13.4	89.3	858	11	CNS0643B
C 40	13.4	89.3	1074	6	AR386605
C 41	13.4	89.3	1104	8	AB189674
C 42	13.4	89.3	1238	1	AB174823
C 43	13.4	89.3	1281	9	BC064028
C 44	13.4	89.3	1404	3	AF026516
C 45	13.4	89.3	1539	6	AX568254

## ALIGNMENTS

RESULT 1	AY547458	3959 bp	RNA	linear	VRL 04-AUG-2004
LOCUS	AY547458				
DEFINITION	Avian orthoreovirus inner capsid protein lambda-A gene, complete cds.				
ACCESSION	AY547458				
VERSION	AY547458.1	GI:47420812			
KEYWORDS	Avian orthoreovirus				
SOURCE	Avian orthoreovirus				
ORGANISM	Virus; dsRNA virus; Reoviridae; Orthoreovirus.				
REFERENCE	1. (bases 1 to 3959)				
AUTHORS	Touris-Otero, F., Cortez-San Martin, M., Martinez-Costas, J. and Benavente, J.				
TITLE	Avian Reovirus Morphogenesis Occurs Within Viral Factories and Begins with the Selective Recruitment of signans and lambda to muns Inclusions				
JOURNAL	J. Mol. Biol. 341 (2), 361-374 (2004)				
PubMed	15276829				
REFERENCE	2. (bases 1 to 3959)				
AUTHORS	Cortez-San Martin, M., Touris-Otero, F., Martinez-Costas, J. and Benavente, J.				
TITLE	Direct Submission				
JOURNAL	Submitted (13-FEB-2004) Biología, Universidad de Santiago de Compostela, Facultad de Farmacia Campus Sur s/n, Santiago de Compostela, La Coruña 15782, Spain				
FEATURES	Location/Qualifiers				
source	1..3959				
	/organism="Avian orthoreovirus"				
	/mol_type="genomic RNA"				
	/strain="G1133"				
	/db_xref="taxon:38170"				
	/segment="L1"				
	/country="USA"				
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(without alignments)  
10487.183 Million cell updates/sec

Title: US-10-750-976-36

Sequence: 1 agatcmtaancatccacagagagatctgatg 34

Scoring table: IDENTITY NUC  
Gapop 10.0, Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database: GenEmbl:  
1: gb\_da:  
2: gb\_hcg:  
3: gb\_in:  
4: gb\_om:  
5: gb\_ov:  
6: gb\_pac:  
7: gb\_pl:  
8: gb\_pl:  
9: gb\_pr:  
10: gb\_ro:  
11: gb\_sts:  
12: gb\_sy:  
13: gb\_un:  
14: gb\_vl:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	26	76.5	4196	6	AR483257
2	22.2	65.3	349	6	CO477694
3	22.2	65.3	400	6	CO498897
4	22.2	65.3	400	6	CO507866
5	22.2	64.7	229957	10	AL670231
6	21.6	63.5	639	11	BV073720
7	21.6	63.5	191804	2	CR385041
8	21.6	63.5	199321	2	AC141872
9	21.6	63.5	319737	2	AC126267
10	21.4	62.9	246739	2	AC133052
11	21.2	62.4	32	6	AI8778
12	21.2	62.4	102	6	AI8323
13	21.2	62.4	161	6	AI13979
14	21.2	62.4	161	6	AI13980
15	21.2	62.4	3712	6	AI49887
16	21.2	62.4	3754	6	AI37074
17	21.2	62.4	3754	6	AI42478
18	21.2	62.4	3754	6	AR257551
19	21.2	62.4	3754	6	AR453380

20	21.2	62.4	3769	6	A37075	A37075 Sequence 18
21	21.2	62.4	3769	6	A49988	A49988 Sequence 5
22	21.2	62.4	3769	6	AR453381	AR453381 Sequence
23	21.2	62.4	4366	6	AR42484	AR42484 Sequence 12
24	21.2	62.4	4366	6	AR257557	AR257557 Sequence
25	21.2	62.4	4378	6	AR42481	AR42481 Sequence 9
26	21.2	62.4	4378	6	AR257554	AR257554 Sequence
27	21.2	62.4	4378	6	AC137111	AC137111 Sequence
28	21.2	61.8	139391	9	AC007239	AC007239 Homo sapi
29	21.2	61.8	139391	9	AC128753	AC128753 Rattus no
30	21.2	61.8	188044	2	AC128753	AC128753 Rattus no
31	21.2	61.8	191583	10	AC134166	AC134166 Rattus no
32	21.2	61.8	226611	10	AC122878	AC122878 Mus muscu
33	21.2	61.8	235803	2	AC097591	AC097591 Rattus no
34	21.2	61.8	248663	2	AC097854	AC097854 Rattus no
35	21.2	61.8	250338	2	AC130248	AC130248 Rattus no
36	21.2	61.8	254454	2	AC121447	AC121447 Rattus no
37	21.2	61.8	260165	2	AC137402	AC137402 Rattus no
38	21.2	61.8	266045	2	AC142860	AC142860 Macaca mu
39	21.2	61.8	318115	2	AC098550	AC098550 Rattus no
40	20.6	61.2	71588	2	AC144909	AC144909 Mus muscu
41	20.6	60.6	651	11	G57834	G57834 SHGC-103587
42	20.6	60.6	700	6	AX182888	AX182888 Sequence
43	20.6	60.6	1204	10	MMKER47R	MMKER47R
44	20.6	60.6	1232	10	BC060286	BC060286 Mus muscu
45	20.6	60.6	4678	10	MMU13921	MMU13921 Mus muscu
			5632	9	HSM802171	HSM802171 Homo sapi

## ALIGNMENTS

RESULT 1	AR483257	4196 bp	DNA	linear	PAT 14-MAY-2004
LOCUS	AR483257				
DEFINITION	Sequence 1 from patent US 6703233.				
ACCESSION	AR483257				
VERSION	AR483257.1	GI:47245788			
KEYWORDS					
SOURCE	Unknown.				
ORGANISM	Unknown.				
REFERENCE	1 (bases 1 to 4196)				
AUTHORS	Galen, J.R.				
TITLE	Plasmid maintenance system for antigen delivery				
JOURNAL	Patent: US 6703233-A 1 09-MAR-2004;				
FEATURES	Location/Qualifiers				
source	1..4196				
ORIGIN	/organism="unknown"				
	/mol_type="genomic DNA"				

Query Match 76.5%, Score 26, DB 6, Length 4196;  
Best Local Similarity 96.3%; Pred. No. 0.16;  
Matches 26, Conservative 0, Mismatches 1, Indels 0, Gaps 0;

Qy	8	TTAATCATCCACAGAGATCTTGATG	34
Db	470	TTAATCATCCACAGAGATCTTGATG	496
RESULT 2			
CO477694			
LOCUS	CO477694	349 bp	DNA
DEFINITION	Sequence 9561 from Patent WO0160860.		linear
ACCESSION	CO477694		PAT 30-JAN-2004
VERSION	CO477694.1	GI:41443313	
KEYWORDS			
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Mammalia; Butheria; Primates; Catarrhini; Hominiidae; Homo.		
REFERENCE	Schlegel, R., Endege, W.O. and Monahan, J.B.		
AUTHORS	1		

